09/881569

FILE 'REGISTRY' ENTERED AT 14:29:32 ON 15 NOV 2002 L1 0 S BTS.PCGAVMILYFHKWR/SQSP

L2 0 S PCGAVMILY/SQSP

FILE 'HOME' ENTERED AT 14:32:35 ON 15 NOV 2002

Searcher: Shears 308-4994

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd. J)

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence of Gly(15	Amino acid sequenc	Tissue factor path	Sphingolipid ceram	Sphingolipid ceram	Protein of Mez2 (M	Human ORFX protein	Zea mays protein f	Arabidopsis thalia	Arabidopsis thalia	Description

Shrimp White Lactococcus Novel human Novel human

ALIGNMENTS

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RESULT 2
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hybridisation assay; ge
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promoter;
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990S-0144332.
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990S-0144833.
990S-0144834.
990S-0144884.
990S-0145086.
990S-0145086.
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AAG26837
ID AAG2
XX
AAC AAG2
XX
AC AAG2
XX
AC AAG2
XX
DE Zea
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Prot
KW Prot
Cern
XX
26a
XX
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PR 06-8
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Best Loc
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05-MAR-1999;

23-MAR-1999;

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01-APR-1999;

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26-MAY-1999;

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28-OCT-1999;
29-OCT-1999;
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8; Conservative
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99US-0121825.

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where x is 1-11491 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ
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                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
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                                                                                                             UNIM)
                                                                                                                                      (WISC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                Kaeppler SM,
                                                                                                                                                                                                    17-JUL-2000;
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                                                                                                                                                                                                                                                                                          24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, diabetes mellitus, systemic on, hypothyroidism, cholesterol ester deficiencies and disorders, infectious such as multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patent did not form part of the printed in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polycomb group; PcG; Maize E(z)-like;
improvement; agronomic trait;
i; screening; affinity chromatography;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z 4
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                                                                    ris
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                                                                    Phillips RL;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to plant genetic engineering. More specifically, the invention relates to isolated and purified polycomb group (PcG) genes comprising a sequence of 3180 and 3030 by respectively, defined in the specification, or its conservatively modified and polymorphic variants. The PcG genes of the invention are useful in constructing recombinant expression cassettes which can be introduced into a desired plant, to produce a transgenic plant. Promoters derived from the Mezl or Mezl genes are useful to direct expression of heterologous sequences. The committed variants of the PcG genes are useful for generating or selecting antibodies immunoreactive to the non-variant polypeptide and to follow the segregation of chromosome regions and in marker assisted selection methods for crop improvement. Mezl and Mezl proteins can be used to repress the expression or prevent the expression of a desired target gene expression in plants to create novel plants having improved agronomic traits. Protein derived from a PcG gene of the invention is useful as an immunogen for producing monoclonal or polyclonal antibodies which are useful for screening plants for the expression of a Mezl or Mezl colypeptide, and for affinity chromatography for isolating a Mezl or Mezl colypeptide. This sequence represents the protein of Mezl of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polycomb group nucleic acids and polypeptides from maize useful for producing transgenic plants and to repress expression or prevent the expression of a desired target gene in specific tissue in plants
                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                     Sphingolipid
                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2002
New polypeptide
                                                                                                                                                                   26-SEP-2001;
                                                                                                                                                                                                 04-APR-2002
                                                                                                                                                                                                                                                             Shewanella alga.
                                                                                                                                                                                                                                                                                       Sphingolipid ceramide deacylase; nootropic; neuroprotective; cytostatic; vulnerary; neurodegenerative disease; leukaemia; wound; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                  AAU78464;
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                                                                            Z,
                              2002-340011/37.
)B; ABK47644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENKKPCGHLCYLRFPQWR 334
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                                                                                                                                     2000;
                                                                           Furusato
                                                                                                       TAKARA
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                                                                                                                                                                   2001WO-JP08344.
                                                                                                                                                                                                                                                                                                                                       ceramide
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 with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.1%; 38.9%;
sphingolipid
                                                                          Sueyoshi
                                                                                                                                                                                                                                                                                                                                     deacylase
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ceramide
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deacylase
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activity
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RESULT 7
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ID AAU7
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Best Local
                                                                                                                                                                               New polypeptide with sphingolipid ceral encoded gene, applicable in studying s sphingolipid and its engineering for toneurodegenerative diseases and leukaem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a polypeptide with sphingolipid ceramide deacylase activity and its encoding nucleic acid. The polypeptide and its encoded gene are applicable in studying structure and function of sphingolipid and its engineering for treatment of e.g. neurodegenerative diseases, leukaemia and wounds. The present sequence represents the amino acid sequence of sphingolipid ceramide deacylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoded gene, applicable in studying strusphingolipid and its engineering for treaneurodegenerative diseases and leukaemia
                                                                                    sphingolipid
diseases, leu
                                                                                                          The invention relates to a deacylase activity and its encoded gene are applicable
                                                                                                                                                                                                                                                       WPI;
                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Shewanella alga.
                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sphingolipid ceramide
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                                                                           amino
                                                                                                                                                           Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sphingolipid
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DB; ABK47651.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSZPCGAVMILYFH----KWR 18
                                                                         acid
                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                                                                                       TAKARA SHUZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 34.8
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Page
                                                                                                                                                                                                                                                                               Furusato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                     leukaemia
                                                                        sequence
                                                                                                                                                          Page 76-78; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative
                                                   992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954 AA;
                                                                                                           are applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ceramide deacylase
                                                                                                  and its
                                                                                                                                                                                                                                                                                                                                                    2001WO-JP08344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                     and wounds. The of sphingolipid
                                                                       s to a polypeptide with sphingolipid ceramide nd its encoding nucleic acid. The polypeptide and its licable in studying structure and function of engineering for treatment of e.g. neurodegenerative and wounds. The present sequence represents the of sphingolipid ceramide deacylase #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.2%;
34.8%;
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Pred.
                                                                                                                                                          Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; neuroprotective; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structure and function of treatment of e.g.
DB 23; LG
1.6e+02;
                                                                                                                                                                                           mide deacylase activity and tructure and function of reatment of e.g.
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1.5e+02;
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia; wound; enzyme.
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Query Match Best Local S Matches 8

Similarity 8; Conserv

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RESULT 8
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                                                                                                                                                Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious cc complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The protein sequence of human placental bikunin has been isolated (see AAB14159). Placental CC bikunin is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung CC airways. Therefore, placental bikunin may be used for treating lung caused by retention and accumulation of mucus. The present sequence is a known Kunitz-like domain and was used to identify the CC Kunitz-domains of placental bitomain
                                                       Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                  Stimulating mucociliary clearance rate of mucus and sputum in lairways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mucociliary dysfunction; mucus; sputum; chronic obstructive lung disease; chronic bronc BE; asthma; cystic fibrosis; CF; bacterial infe Kunitz-type serine protease inhibitor; chronic tissue factor pathway inhibitor precursor.
                                                                                                                Sequence
                                                                                                                                             Kunitz-domains of
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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17-NOV-1999;
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 PCRALLLRYYYRYR
                          PCGAVMILYFHKWR
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                                                        Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poll
                                                                                                                  57 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Page 22;
                                                      Conservative
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99US-0441966.
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 25
                           18
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                                                                    41.2%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB,
                                                                                                                                             bikunin.
                                                      Score 42; DB Pred. No. 11; 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor WJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chronic bronchitis; CB; Bronchiectasis;
macterial infection; placental bikunin;
.tor; chronic sinusitis; glue ear;
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                                                                                   21;
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                                                       2;
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AAP50700
ID AAPS
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AAY35526
RESULT 10
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                                                                                                                                                                                                                    Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                            frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                             Protease inhibitor; a kallikrein inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY35526 standard;
                                                             Sequence
                                                                                 28-NOV-1991
                                                                                                      AAP50700;
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                              Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sinusitis; purulent of vaccine; neutralising
                                                                                                                          AAP50700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY35526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory
                                                                                                                                                                               ~)
                                                                                                                                                                                                 2
                                                                                                                                                                        TTEPCSSIHISLNNDWR
                                                                                                                                                                                                TSZPCGAVMILYFHKWR 18
                                                                                                                                                                                                                                                                                                                                                                                                        1278-1279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                    similarity 35.3%;
6; Conservative
                                                             of.
                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                             223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                           Gly(15)-Aprotinin.
                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-IB01890.
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                             antitrypsin
r; elastase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      otitis media;
                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitope
                                                                                                                                                                             23
                                                                                                                                                                                                                    Score 42; DB Pred. No. 48; 5; Mismatches
                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                        1912pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                          Š
                              inhib
                             activity; shock therapy;
inhibitor; arthritis therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bronchitis; heart disease; sarcoidosis;
s; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                               2; DB 20;
lo. 48;
                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neumoniae
                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                        Length 223;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                     0
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                      0
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RESULT 11
AAW35008
ID AAW35
XX
AC AAW35
XX
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8
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventors claim homologues of aprotinin in which 15-Lys has been replaced by one of (all L forms where applicable) Gly,Ala,Val,Leu, Ile,Met,Arg, alpha-aminobutyric acid, norvaline, Nle, dehydroalanine or homoserine. Also new are the intermediate derivs. in which (1) 15-Lys is replaced by one of the specified AAs or their alkyl esters and any additional COOH in side chains or terminal posn. are partly or completely esterified; (2) the bond between 15-Lys and 16-Ala is open and only 15-Lys COOH is in free form, all other side chain COOH (3- and 50-Asp; 7- and 49-Glu) and C-terminal COOH (58-Ala) are present as alkyl esters; (3) the 15/16 bond is broken; 15-Lys is absent, the side chain and terminal COOH are esterified and only 14-Cys has a COOH in free form.
                                                                                                                                                                    Endoglucanase; cellulase; carboxymethylcellulose; cellulose; biomass; beta-1,4-glycosidic bond; hydrolysis; saccharification; thermostable enzyme; thermophilic; glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new
                                                                                                                                                                                                                                                                  AAW35008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1983;
28-JUL-1983;
                                                                                                                           WO9744361-A1
                                                                                                                                                   Vibrio
                                                                                                                                                                                                                                                                                         AAW35008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tschesche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUL-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP132732-A.
                                                                              22-MAY-1997;
                                                                                                     27-NOV-1997.
                                                                                                                                                                                                                    Vibrio harveyi endoglucanase
                                                                                                                                                                                                                                           21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARB ) BAYER
                                  (RECO-)
                                                        22-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aprotinin derivs. with intermediate, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1985-039382/07.
                                                                                                                                                                                                                                                                                                                                                                       PCGAVMILYFH 15
                                                                                                                                                                                                                                                                                                                                                PCGARIIRYFY 23
                                                                                                                                                  harveyi (Clone 91GP2).
                                                                                                                                                                                                                                                                                                                                                                                             Similarity 63.77; Conservative
                                  RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock
                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ή
                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wenzel
                                                        96US-0651572
                                                                              97WO-US08793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83DE-3339693
83DE-3327277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84EP-0108293
                                                                                                                                                                                                                                                                                        Protein;
                                  BIOCATALYSIS
                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                      40.2%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmuck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-lysine
15 protease
                                                                                                                                                                                                                                                                                         504 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB Pred. No. 17; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replaced by inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schnabel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ħ
                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aminoacid
e.g. for
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                            0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 12
AAW59445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1997;
29-JUL-1996;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has homology to an endoglucanase of an AAW34985). It can be produced from na host cells, especially prokaryotic hosplasmid or virus-derived vector incluces (see AAT94216). 24 Endoglucanases (see They can be used to degrade cellulose to degr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoglucanase(s), preferably form archael bacterium, AEPII la useful to degrade carboxymethylcellulose and hydrolyse of beta-1,4-glycosidic bonds in cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biomass into fuels and chemicals, animal feed, waste treatment, and industries for the clarification a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                        The sequence
                                                                                                                                                                                                                                                                           WPI; 1998-159149/14.
N-PSDB; AAV35030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare MLO
                                                                                                            Claim 8;
                                                                                                                                                                                                                      New isolated
                                                                                                                                                                                                                                                                                                                                                           Bueschges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9804586-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW59445
                                                                                                                                                                   resistance
                                                                                                                                                                                                                                                                                                                                                                                                               (INNE-) INNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of hydrolysing the beta-1,4-glycos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mildew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-018435/02.
DB; AAT94216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDGGVVVGYWHNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCGAVMILYFHKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 46.3
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig
                                                                                                        Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 AA;
                                                                                                                                                                                                                    Mlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1X; 164pp;
   negative regulatory
                                                       is that encoded by a
                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                    Mlo gene of
transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                 CENT
                                                                                                                                                                                                                                                                                                                                                           Panstruga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97GB-0004789.
96GB-0015879.
96GB-0022626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-GB02046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nprises an endoglucanase of Vibrio harveyi at is capable of degrading carboxymethylcellulose ing the beta-1,4-glycosidic bonds in cellulose. It an endoglucanase of archaebacterium AEPIIIa (see can be produced from native cells or from recombinant exially prokaryotic host cells transformed with a recially prokar
                                                                                                        150pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                 INNOVATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.2%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                           ℷ
                                                                                                          English
                                                                                                                                                                                        barley
plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544
                                                                                                                                                                                                                                                                                                                                                           Schulzele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                 LTD
                                                                                                                                                                                            which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misma
                        func
homologue of the MLO gene, wild-type function on a pathogen defence response, ce response in the absence of pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N A
                                                                                                                                                                                                                                                                                                                                                                                                                 ΙŌΓ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tches
                                                                                                                                                                                                                                                                                                                                                             fert PMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                 HN.
                                                                                                                                                                                        to develop products for the have increased pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
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defence

<u>ب</u>

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RESULT 13
AAU42094
ID AAU42
XX
AC AAU42
XX
AC AAU42
XX
AC AAU42
XX
DT 27-FE
XX
DE Prop1
XX
SAPHC
KW LINFLL
KW INFLL
KW derma
XX
PN WO20C
XX
PN WO20C
XX
PD 01-NC
XX
PF 20-AF
PR 02-JL
PR 07-JL
            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                    sequences AAU39105-AAU68017 represent Propionibacterium aches immunogeni polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Down-regulation or out-competition of MIO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with
                                                                                                                                                                                                                                                                                 Propionibacterium acnes vaccinating against and treating acne vulgaris
            downregulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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2000US-208841P.
2000US-216747P.
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e J, Zhang Y,
          expression
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y be user acnes proteins. These acnes proteins. These
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                                                                                                                                                                                                                                                                                                   polypeptides and nucleic diagnosing infections, ex
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Jen S, Carter D;
                                                                                                                                                                                                                                                     1069pp; English.
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1; Mismatches
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        polypeptides
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are used in
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RESULT 14
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Best Local :
                                                                                        monocytogenes EGD-e (see ABA03041). The genome sequence of Listeria it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a sequence in L.
                                                encoded by the genome sequence of the expressed from the genome sequence are antibodies, identification of L. monofor biosynthesis and him.
                      B12. The genome sequence and protein selecting compounds that regulate gen
                                                                                                                                                                                                                  Genomic sequence for Listeria and prevention of Listeria and related polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                   Rose
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Perez-Diaz J,
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              and modulate
                                       for biosynthesis and biodegradation, B12. The genome sequence and protein
                                                                                                                                                                                           Claim
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Daniels J,
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                                                                                                                                                                                                                                                                                                               J, Baquero
De Pablos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 AA;
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proteins
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Baquero F,
Pablos B,
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              monocytogenes-related diseases.
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ann E, Hain T, B
ero F, Garcia Del
los B, Wehland J,
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Pred.
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d relate
                       e of the present invention. Proteins sence are useful for raising specific L. monocytogenes and related organisms, and dation, especially biosynthesis of Vitamin proteins encoded by it are also useful for late gene expression and cell replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z 4
                                                                                                                                                                                                                                 togenes, useful e.g. for treatment ed bacterial infections, and
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l Portillo F, Gomez-Lopez N;
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o. 1.9e+02;
are useful in pharmaceutical and
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              In addition,
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RESULT 15
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Matches 6
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15-JUN-1990;
17-JUN-1991;
13-APR-1995;
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Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                           This invention describes novel transgenic mice expressing proteins related to the pathology of Alzheimer's disease and which provide models for studying potentially therapeutic compounds. The transgenic mice contain a DNA sequence encoding a beta-amyloid precursor protein (APP) and a nerve tissue specific promoter operably linked to the beta-APP allowing its expression to form beta-amyloid protein deposits in the molecular mechanisms involved in the synthesis of and, more importantly, inhibiting the synthesis and deposition of beta-amyloid proteins (most importantly in the brain where plaque formation is associated with Alzheimer's disease) by inhibiting production and/or increasing cleavage after production. The transgenic animals provide useful models for studying the in vivo relationships of the proteins to each other and to other compounds being tested for their usefulness in treating Alzheimer's
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nerve tissue specific
plaque formation; trea
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                                                            disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic mice useful for studying compounds the treatment of Alzheimer's disease
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90US-0538857.
91US-0716725.
95US-0422333.
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Similarity 63.6%;
7; Conservative
25
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Search completed: November 15, Job time : 36 secs 2002, 11:44 :12

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Match
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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US-08-422-333-14
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US-08-632-021-2
US-08-443-976-61
US-08-443-976-61
US-08-358-160-111
US-08-484-938-4
US-08-791-1158-25
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US-08-484-1588-4
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US-08-484-1596A-4
US-08-480-150A-4
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37.829 Million cell updates/sec
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Sequence 112, App Sequence 14, Appl Patent No. 5187153 Patent No. 5220013 Patent No. 5220013 Patent No. 5223482 Patent No. 5466783 Sequence 61, Appli Sequence 61, Appli Sequence 115, Appli Sequence 111, App Sequence 111, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 23, Appli Sequence 25, Appli Sequence 25, Appli Sequence 4, Appli
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Patent No.
Patent No.
Patent No.
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US-08-358-160-112
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 Patent No.
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                                                                                                                                                                                                                                                                      COUNTRY:
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ALIGNMENTS

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APPLICANI: ROBERIS,
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMA!
TITLE OF INVENTION: DOMAINS THAT IN
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
ADDRESSEE: BROWDY AND NEIMARK
TOTAL 419 Seventh Street, N.W.
                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION NUMBER: US 08/09,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: COOPET, IVET P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
NAME: Cooper, Iver I
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMI
TELECOMMUNICATION INFOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112, Application 5. 5663143
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    INFORMATION:
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                     NUMBER:
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IBIT HUMAN NEUTROPHIL ELASTASE
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; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-112
           RESULT 3
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US-08-422-333-14
Patent No.
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                                                                                                                                                                                                                                                NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSEE: Scios, Inc. STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                       Local
                                                                                                                                                                                                        LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 13-AP
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2450 Bayshore Parkway
Jountain View
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A
; TITLE OF INVENTION: DNA SEC
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
                                                                                         RESULT 5
5223482-24
; Patent No.
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5220013-25
; Patent No.
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BARBARA
TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5187153-22
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                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/44
FILING DATE: 30-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
                                                                        APPLICANT: SCHILLING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 361,912 FILING DATE: 06-JUN-1989 APPLICATION NUMBER: 359,911 FILING DATE: 12-MAY-1989 APPLICATION NUMBER: 87,002 FILING DATE: 18-AUG-1987 APPLICATION NUMBER: 8,810 FILING DATE: 30-JAN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
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: DNA SEQUENCE USE
                                                                                                                                                                                                                                                39.2%;
63.6%;
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63.6%;
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                                                                            W. ; PONTE
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Pred.
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No. 35;
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No. 35;
Natches
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                                                                         PHYLLIS A.; CORDELL,
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RESULT 6
5466783-5
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US-09-632-021-2
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wun, Tze-Chein,;Kretzmer, Kuniko K.;Broze, George J. Jr.
TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                   Sequence 2, Application US/09632021
Patent No. 6406896
GENERAL INFORMATION:
APPLICANT: Reznikoff, William S
APPLICANT: Naumann, Todd A
                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
           PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 5
                                                        CURRENT APPLICATION NUMBER: US/09/632,021 CURRENT FILING DATE: 2000-08-02
                                                                                     APPLICANT: Naumann, Todd A
TITLE OF INVENTION: Transposase Enzyme and Method for
FILE REFERENCE: 960296.96471
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/93
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,280
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 123,753
FILING DATE: 23-NOV-1987
APPLICATION NUMBER: 77,366
FILING DATE: 23-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 26 CURRENT APPLICATION DATA:
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mes 7; Conserv
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63.6%;
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                                            60/146686
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Pred. No.
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Pred. No.
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; TYPE: PRT
; ORGANISM: Transposon Tn5
US-09-632-021-2
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Best Local Similarity
Thehes 8; Conserve
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GENERAL INFORMATION:
                                                                                                    FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NOTWOOD
                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/DK88/00138 FILING DATE: 28-AUG-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
                           FILING DATE: 12-JUN-
PRIOR APPLICATION DATA:
                                                                        FILING DATE: 19-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                              APPLICATION NUMBER: US 07/466,408 FILING DATE: 21-JUN-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                          APPLICATION NUMBER: PCT/DK89/00096 FILING DATE: 25-APR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRE
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                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 19930
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COMPUTER: IB
 APPLICATION NUMBER: FILING DATE: 01-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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10174-6201
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Bregengaard, Claus
No. 5591603ris, Fanny
Petersen, Lars C.
VENTION: Process for the Preparation of Aprotinin
VENTION: and Aprotinin Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diness, Viggo
No. 5591603rskov-Lauritser
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No. 5591603ris,
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                       JMBER: US 07/598,337
19-NOV-1990
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19930623
MBER: PCT/DK91/00299
01-OCT-1991
                                       MBER: DK 1118/91
12-JUN-1991
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Pred. No.
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tches 4; Indels
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US-08-443-976-61
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US-08-084-718-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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Best Local
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                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,976
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-10-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-200-1993
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APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-U:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-867-0123
TELEFAX: 212-867-0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              COMPUTER READABLE MEDIUM TYPE: FI
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TOPOLOGY: 1:--
                              PRIOR APPLICATION DATA:
                                                                        FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
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APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1992
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CITY: 1
STATE:
                                               FILING DATE:
                                                             APPLICATION NUMBER:
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NY: United States
10174-6201
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No. 5618915rskov-Lauritsen, Leif
Christensen, Niels D.
Bregengaard, Claus
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No. 5618915ris, Kjeld
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NUMBER: P
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                                        UMBER: DK 2254/88
26-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                    5618915ris, Fanny
ersen, Lars C.
ION: Process for the Preparation of Aprotinin
ION: and Aprotinin Analogs
                                                                                                                                                                                                                                                                                               FORM:
                                                                                                                                                                                                                                                                                                                                                                                      56189150 No.
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             PCT/DK88/00138
                                                                                                                                                                                                                                                                                                                             of America
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                                                                                                                                                                                                                                                                                                                                                                         5618915d1sk of No.
s, 62nd Floor
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US-08-443-977-61
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Best Local S
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FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-867-029: INFORMATION FOR SEQ ID NO
                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/827,687 FILING DATE: 29-JAN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/024,925 FILING DATE: 26-FEB-1993 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NOTHING
                                                                                                          NUMBER OF SEQUENCES: 8
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FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
               COMPUTER READABLE
                                                                                                                                      TITLE OF INVENTION:
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FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
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                         COUNTRY: United States ZIP: 10174-6201
                                                      STATE:
                                                                     CITY:
                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                           66
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                                                                                             ADDRESSEE:
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                                                     New York
                                                                                                                                                                                                                                                                                                      Application US/08443977
                                                                                                                                                                   No. 56210/4150.
Christensen, Niels D.
Bregengaard, Claus
No. 5621074ris, Fanny
                                                                              E: No. 5621074
405 Lexington
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212-867-0298
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No. 5621074ris, Kjeld
Diness, Viggo
No. 5621074rskov-Lauritsen, Leif
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No. 84;
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IBM PC

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RESULT 11
US-09-499-302A-9
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                                             Sequence 9, Application US/09499302A Patent No. 6369212
                                GENERAL
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Best Local
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FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ
 APPLICANT:
                 APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U:
FILING DATE: 19-NOV-1:
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PRIOR APPLICATION NUMBER: USE PRICE PAPPLICATION NUMBER: USE PILING DATE: 21-JUN-1
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 12-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                 INFORMATION:
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7; Conservative
BOUNG-JUN, OH MOON, KYUNG KO
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212-867-0298
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                                                                                                                                                                                                         Mismatches
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; LOCATION: (394)
; OTHER INFORMATION:
US-09-499-302A-9
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US-08-358-160-115
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Best Local
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CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
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NAME/KEY: MOD_RES
LOCATION: (324)
OTHER INFORMATION:
NAME/KEY: MOD_RES
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OTHER INFORMATION: (NAME/KEY: MOD_RES
LOCATION: (62)
OTHER INFORMATION: (NAME/KEY: MOD_RES
LOCATION: (243)
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LOCATION: (246)
COCCUTE INFORMATION: (246)
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TYPE: PRT
ORGANISM:
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NAME/KEY: MOD_RES
LOCATION: (253)
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                                                                                                                                                                                  TITLE OF
       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                           NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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CITY: W
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ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
                                                                                                                                                                                                                                                                                              Application US/08358160
                                                                                              USA
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                                                                                                                                                            ADDRESS
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                                                                                                                                 // ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5196
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TELEFAX: 248633
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TVPE: amino acid
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Best Local Similarity
Matches 7; Conser
                                                                 Matches
                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                             Sequence 5196, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5196
LENGTH: 346
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                09-134-001C-5196
                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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PRIOR APPLICATION NUMBER FILING PARTS
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
 129
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NUMBER: 28,005
KET NUMBER: LEY
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                                                                             Score 37.5; DB 4; Pred. No. 3.7e+02;
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RESULT 14
US-08-358-160-110
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; Patent No. 5663143
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/358,160 FILING DATE: 16-DEC-1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: LE TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/664,989 FILING DATE: 01-MAR-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/133,031 FILING DATE: 13-OCT-1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-SEP-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                         MOLECULE TYPE:
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CITY: Washington
STATE: District
13
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PCKARMIRYFY 23
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                                                               Similarity 7; Conserv
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ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
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linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                        protein
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DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
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Pred. No
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atches 3; Indels
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TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-111
Search completed: November 15, 2002, 11:45:31 Job time : 15 secs
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Best Local S
Matches 7
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FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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CITY: Washington
STATE: District of Columbia
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419 Seventh Street, N.W. Suite 300
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LADNER, ROBERT C.
GUTERMAN, Sonia K.
ROBERTS, Bruce L.
MARKLAND, William
KENT, Rachel B.
VENTION: ENGINEERED HUMAN-DERIVED KUNITZ
VENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
EQUENCES: 234
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1: /cgn2_6
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Match
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Maximum Match 100%
Listing first 45 summaries
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: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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US-09-903-170C-7
0 US-09-903-180B-7
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                      Sequence 2, Appli
Sequence 1, Appli
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Sequence 48038, A
Sequence 246, App
Sequence 246, App
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Sequence 8, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 9, A Sequence 17, Sequence 9,
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1-569A ce 1, No. U I INFO	P P	Match Local Simi	ULT 1 09-881-569A-2 equence 2, Appliatent No. US2002 ENERAL INFORMATI APPLICANT: KHANN TITLE OF INVENTI TITLE OF INVENTI TITLE APPLICATI CURRENT APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR FILING DAT PRIOR FILING DAT PRIOR FILING DAT OF SEQ ID NO 2 LENGTH: 18 TYPE: PRT ORGANISM: Arti FEATURE: OTHER INFORMATI OTHER INFORMATI OTHER INFORMATI OTHER INFORMATI		33333333333333333333333333333333333333
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)98	18	80 80	988 9988 998 998 998 998 998 998 998 99		100 100 100 100 100 100 100 100 100 100
/09881569A		; Score 102; DB 10; ; Pred. No. 3.4e-10; 0; Mismatches 0;	31569A DIPPEPTIDE-K OBTAINE CESS FOR THE EXTRAC 5/09/881,569A -14 /DEL/99 /DEL/99 /DEL/99 /DEL/99 /DEL/99	ALIGNMENTS	US-09-903-187A-9 US-09-903-171A-9 US-09-903-188A-9 US-09-903-323A-9 US-09-903-325A-9 US-09-903-325A-9 US-10-028-051-4 US-09-870-379-2 US-10-001-879-194 US-09-764-762-4 US-09-986-975A-7 US-09-9864-761-44551 US-09-9863-322-5 US-09-843-676-4 US-09-843-676-4 US-09-843-676-4 US-09-949-192-45 US-09-949-192-45 US-09-949-192-45 US-09-964-877-1085 US-09-764-877-1085 US-09-7711-5 US-09-7711-5
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TITLE OF INVENTION: PROTEIN/POLYPEPTIDE

-K OBTAINED FROM MOMORDICA CHARANTIA

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RESULT 4
US-09-864-761-48038
; Sequence 48038, Application
; Patent No. US20020048763A1
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GENERAL INFORMATTON:
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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Best Local
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           APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED:
TITLE OF INVENTION: GENE EXPRESSION ANALY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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CURRENT FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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Hanzel, David K.
Chen, Wensheng
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NUMBER:
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Pred. No.
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Pred. No. 18;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic
FILE REFERENCE: PT214
                             SOFTWARE: PatentIn Ver.
SEQ ID NO 484
LENGTH: 74
TYPE: PRT
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Best Local
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SOFTWARE: Annomax Sequence:
SEQ ID NO 48038
LENGTH: 39
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NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
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PRESENTE TO THE PROPERTY OF THE PR
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R APPLICATION NUMBER: PCT/US01/00664
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00669
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00665
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/US01/00668
R FILING DATE: 2001-01-30
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R APPLICATION NUMBER: PCT/US01/00663
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/0069
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APPLICATION NUMBER: PCT/US01/00667
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US-09-815-242-11466
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US-09-895-913A-246
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APPLICANT:
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Encoding No. U
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
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SOFTWARE: FastSEQ for
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                                       OR APPLICATION NUMBER: 60/191,078
OR APPLICATION NUMBER: 60/191,078
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/207,727
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/
FILING DATE: 2000-11-27
                                      APPLICATION NUMBER:
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5. US20020160456A1
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Zyskind, Judith W
Wall, Daniel
Trawick, John D.
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                                                                                                                                                                                                                            Carr, Grant
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                         NUMBER: 60/242,578
2000-10-23
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63.6%;
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RESULT 8
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: U
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FILING DATE: 2000-12-22
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                                                FILING DATE: 2000-06-30 APPLICATION NUMBER: US | FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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HUMBER: PCT/US01/0066
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WMBER: US 09/632,366
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RESULT 9
US-10-028-051-8
; Sequence 8, Application US/10028051
; Patent No. US20020147329A1
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/028,051

FILING DATE: 19-Dec-2001

CLASSIFICATION CUNKNOWN>

PRIOR APPLICATION DATA:
                                                                                   APPLICATION NUMBER: 08/729,452
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Nell S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH133.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
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LENGTH: 318 amino acids TYPE: amino acid STRANDEDNESS: single
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42.9%;
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ED IN BT474, SIGNAL = 9.2
ED IN BONE MARROW, SIGNAL = 10
ED IN BRAIN, SIGNAL = 9.2
ED IN PLACENTA, SIGNAL = 12
ED IN HELA, SIGNAL = 11
ED IN HBL100, SIGNAL = 10
ED IN ADULT LIVER, SIGNAL = 16
ED IN LUNG, SIGNAL = 13
AN HIT: AW411290.1, EVALUE 5.00e-05
OT HIT: P81274, EVALUE 9.00e-06
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16th Floor
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APPLICANT: Bouwmeester, Tewis
TITLE OF INVENTION: Endoderm, Cardiac and
TITLE OF INVENTION: Factors
FILE REFERENCE: 510015-259
CURRENT APPLICATION NUMBER: US/09/903,170
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 60/020,150
PRIOR FILING DATE: 1996-06-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 323
TYPE: PRT
ORGANISM: Mouse FRZB-1
US-09-903-170C-7
                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

APPLICANT: Bouwmeester, Tewis

TITLE OF INVENTION: Endoderm, Cardiac and

TITLE OF INVENTION: Factors

FILE REFERENCE: 510015-256

CURRENT APPLICATION NUMBER: US/09/903,180

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 3.0
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SEQUENCE DESCRIPTION:
US-10-028-051-8
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US-09-903-170C-7
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SEQ ID NO 7
LENGTH: 323
TYPE: PRT
ORGANISM: Mouse FRZB-1
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Best Local S
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QGCEPILIKYRHSW
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SOFTWARE: FastSEQ for Wir
SEQ ID NO 7;
LENGTH: 323;
TYPE: PRT;
ORGANISM: Mouse FRZB-1
US-09-903-171A-7
   RESULT 14
US-09-903-188A-7
; Sequence 7, Application US/09903188A
; Patent No. US20020128439A1
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US-09-903-187A-7
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APPLICANT: Bouwmeester, Tewis
TITLE OF INVENTION: Endoderm, Cardiac and Neu
TITLE OF INVENTION: Factors
FILE REFERENCE: 510015-248
CURRENT APPLICATION NUMBER: US/09/903,187A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/552,988
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: US 08/878,474
PRIOR APPLICATION NUMBER: US 60/020,150
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1996-06-20
NUMBER OF SEQ ID NOS: 10
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SEQ ID NO 7
SEQ TO NO 7
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GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M. APPLICANT: Bouwmeester, Tewis
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TITLE OF INVENTION: Factors
FILE REFERENCE: 510015-260
CURRENT APPLICATION NUMBER: US/09/903,171A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 60/020,150
PRIOR FILING DATE: 1996-06-20
NUMBER OF SEQ ID NOS: 10
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....FLICANT: Bouwmeester, Tewis; TITLE OF INVENTION: Endoderm, Cardiac and Neu; TITLE OF INVENTION: Factors; FILE REFERENCE: 510015-261; CURRENT APPLICATION NUMBER: US/09/903,323A; CURRENT FILING DATE: 2001-07-11; PRIOR APPLICATION NUMBER: US 60/020,150; PRIOR FILING DATE: 1996-06-20; NUMBER OF SEQ ID NOS: 10; SOFTWARE: FastSEQ for Windows Varalle SEQ ID NO 7; LENGTU.
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US-09-903-323A-7
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Search completed: November Job time: 11 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/903,18 CURRENT FILING DATE: 2001-07-11 PRIOR APPLICATION NUMBER: US 60/020,150 PRIOR FILING DATE: 1996-06-20 NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 3
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TYPE: PRT
ORGANISM: Mouse FRZB-1
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TYPE: PRT
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4: pir4:*
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4411.221.1
4411.221.1
4400.221.2
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D84686
T09771
T059572
T30418
AB1793
AH1417
F83000
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T30637
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S45888
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ALIGNMENTS

RESULT 1

B69433
signal-transducing histidine kinase homolog - Archaeogroup - C; Species: Archaeoglobus fulgidus
C; Accession: B69433
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A: Reference number: A69250; MUID: 98049343; PMID: 9389475 gamma-glutamyl carboxylase (EC 4.1.1.-) - bovine
C;Species: Bos primidenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A47439; A38939; B39283; C39283
R;Rehemtulla, A.; Roth, D.A.; Wasley, L.C.; Kuliopulos, A.; Walsh, C.T.; Furie, B.; F
Proc. Natl. Acad. Sci. U.S.A. 90, 4611-4615, 1993
A;Title: In vitro and in vivo functional characterization of bovine vitamin K-depende
A;Reference number: A47439; MUID:93281629; PMID:8506307
A;Accession: A47439
A;Accession: A47439; MUID:93281629; PMID:8506307
A;Cross-references: GB:L09726; NID:93281629; PMID:8506307
A;Cross-references: GB:L09726; NID:9289398; PIDN:AAA30425.1; PID:g289399
A;Cross-references: GB:L09726; NID:g289398; PIDN:AAA30425.1; PID:g289399
A;Accession: A38939
A;Accession: A38939
A;Accession: A38939
A;Accession: A38939
A;Cross-references: GB:M81593: NID:G169744. DIN:AAA30410 1: DIN:G169746
A;Cross-references: GB:M81593: NID:G169744. DIN:AAA30410 1: DIN:G169746
A;Cross-references: GB:M81593: NID:G169744. DIN:AAA30410 1: DIN:G169746 RESULT A47439 Дb A; Status: preliminary; nucleic A; Molecule type: DNA A; Residues: 1-222 < KLE> A;Cross-references: R;Wu, S.M.; Cheung, å A;Cross-references: GB:AE001001; GB:AE0007 Best Loc Matches Query y Match Local Similarity Thes 6; Conserv 204 NEPCGAVFVMEF ω SZPCGAVMILYF Conservative GB:M81593; NID:g162744 W.F.; Frazier, D.; Sta 14 43.1%; 4. Score Pred. Misma Š. 44 1; DB : ; PIDN:AAA30410.1; PID:g162745 fford, D.W. 82; NID:g2689324; PIDN:AAB89779.1; PID:g264 DB 2; Length 222; 2; Indels 0; Gaps 9

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A; Cross-references: GB:M81
A; Accession: C39283
A; Molecule type: protein
A; Residues: 37-50 <WU3>
C; Keywords: carbon-carbon
                                                                                                                                                                                                                 R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chida they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, A; Reference number: A71250; MUID:98332770; PMID:9665876
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G71266
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch R;Kaneko, T.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Nakazaki, N.; Sasamoto, S.; Watanabe, A.; Tabata, M.; Yasuda, M.; Tabata, M.; Yamada, M.; Yasuda, M.; Tabata, M.; Yasuda, M.; Yasuda, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, M.; Yamada, M.; Yasuda, Yasuda, M.; Yasuda, M
                                                                                                                                                                                                                                                                                                                                          C;Accession: G71266
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.(
                                                                                                                                                                                                                                                                                                                                                                                                                 probable ATP dependent nuclease, subunit A - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24 - Jul - 1998 #sequence_revision 24 - Jul - 1998 #text_change 05 - Nov - 1999
C; Accession: G71266
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A; Residues: 1-64 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75469.1;
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: asr3770
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A;Title: Cloning and expression of the cDNA for human gamma-glutamyl carboxylase A;Reference number: A39283; MUID:92086858; PMID:1749935
A;Accession: B39283
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M.; Utterback,
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RESULT 5
D86600
SET domain protein [imported] - Chlamydophila pneumoniae (strain J138)
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C; Accession: D86600
R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349; PMID:10871362
A; Accession: D86600
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-221 <STO>
A; Cross-references: GB:BA000008; NID:g8979252; PIDN:BAA99086.1; GSPDB:GN00142
A; Experimental source: strain J138
C; Genetics:
A; Gene: CPj0878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein CP0991 [imported] - Chlamydophila pneumoniae (strain A C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: B81514
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke P; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Accession: B81514
A;Accession: B81514
set domain protein - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: D72024
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; (
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D72024
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A; Residues: 1-221 <REA>
A; Cross-references: GB: AE002257; GB: AE002161; NID: g7189902; PIDN: AAF38770.1; PID: g718
A; Experimental source: strain AR39, HL cells
C; Genetics:
A; Gene: CP0991
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6; Conser
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ed. No. 52;
Mismatches
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                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                             42; DB
No. 16;
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 Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
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conserved hypothetical protein PA0451 [imported] - Pseudomonas C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change C; Accession: H83589

R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warre adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A; Title: Complete genome sequence of Pseudomonas aeruginosa PA0 A; Reference number: A82950; MUID:20437337; PMID:10984043

A; Accession: H83589

A; Residues: DNA
A; Residues: 1-443 <5TO>
A; Cross-references: GB:AE004482; GB:AE004091; NID:g9946303; PID A; Experimental source: strain PA01 C; Genetics:
A; Gene: PA0451
C; Superfamily: Rhizobium nodulation competitiveness protein nfe
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A;Title: Comparative genomes of Clamydia pneumon A;Reference number: A72000; MUID:99206606; PMID: A;Accession: D72024
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-221 <ARN>
A;Cross-references: GB:AE001668; GB:AE001363; NI
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPn0878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant A; Reference number: AB0502; PMID:11677608
A; Accession: AE0958
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-302 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD03161.1; PID:g16504796
C; Genetics:
A; Gene: STY3944
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A;Cross-references: EMBL:U39725; NID:g384501
A;Experimental source: isolate G37
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Ad M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R., C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycola;Reference number: A64200; MUID:96026346; Pla;Accession: C64248
A:Status: C64248
A; Molecule type: DNA
A; Residues: 70-374 <TIGR>
A; Cross-references: GB:U39730;
A; Experimental source: strain (C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T09771; C64248
R;Fraser, C.M.; Gocayne, J.D.;
, M.; Fuhrmann, J.L.; Nguyen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.; Koo, H.; Moffat, K.S.; Cronin, Leuss, D.; Nierman, W.C.; White, O.; Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable RAD51B-like DNA repair protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mycoplasma genitalium
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
C;Accession: T09771; C64248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphatidate cytidylyltransferase N;Alternate names: CDP-diglyceride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-353 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84686 A;Accession: D84686 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-374 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T09771
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                                                                                                           A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                translated from GB/EMBL/DDBJ
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5; Conserv
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number: 216818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.2%;
illarity 27.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Rounsley, S.D.; Shea, Fat, K.S.; Cronin, L.A.; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE002093;
                              strain G-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R. D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; Merr
                                                                                                                                                                                                                                                                               5; NID:g3845017; PID:g3845030
G37
                                                GB:L43967;
                                                                                                             not
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Pred. No
2; Mismai
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                                                                                                             shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
n, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; DB
                                                                                                                                                                                                                                       Adams, M.D.; Clayton, R.A.; Fleischmann, R. R.; Saudek, D.M.; Phillips, C.A.; Merrick,
                                                                                                                                                    Coplasma genitalium.
                                                NID:g1046149; PIDN:AAB01627.1; PID:g1046154
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                                                                                                              translation not shown
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Mlo-hl protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1
Accession: T05952
;Panstruga, R.
submitted to the EMBL Data Library, May 1997
                                                                                                                                                                                                                                                                                                               chitinase (EC 3.2.1.14) - Lymantria dispar nuclear polyhedrosis virus (Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV)
Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul C; Accession: T30418
R; Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Sl Virology 253, 17-34, 1999
A; Title: Sequence and analysis of the genome of a baculovirus pathogen A; Reference number: Z20836; MUID:99124785; PMID:9887315
A; Accession: T30418
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T30418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-544 < PAN>
A; Cross * references: EMBL: Z95496;
A; Experimental source: cv. Igr1
C; Genetics:
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T05952
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-558 <KUZ>
A;Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70256.1; PID:g3822305
                                                                                                                                                                              A;Description: catalyzes the hydroly A;Pathway: chitin degradation C;Superfamily: Serratia marcescens (C;Keywords: glycosidase; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Map position: 4H
A:Introns: 41/3; 139/3;
C:Superfamily: barley p
RESULT
AB1793
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Best Local S
Matches 10
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Best Local
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                                                                                      SZPCGAVMILYFHKW 17
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                                                            AEPTCKYVAAYFVEW
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pathogen
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                                                                                                                                    40.2%;
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                                                                                                                                    Score 41; DB Pred. No. 54;
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                                                                                                                                                                                                                                                                                                                                                    pathogenic
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completed: me : 17 secs

November

15,

2002,

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C; Genetics:
A; Gene: lin2888
C; Superfamily:
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A;Reference number: AB1077; MUID:21537279; pMID:11679669
A;Accession: AB1793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-575 <GLA>
A;Cross-references: GB:AL592022; pIDN:CAC98114.1; PID:g16415423; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                   A; Gene:
C; Superf
                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-575 <GLA>
A; Cross-references: GB:NC_003210;
A; Experimental source: strain EGD:C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AH1417
ABC transporter (ATP-binding protein) homolog lmo2745 [imported] - Listeria monocytog C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C; Accession: AH1417
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C; Date: 27-Nov-2001 #sequence_revision
C; Accession: AB1793
R; Glaser, P.; Frangeul, L.; Buchrieser,
; Dominguez-Bernal, G.; Duchaud, E.; E
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
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Matches 6
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   GAVMILYFHKWR
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                                                   Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 50.06; Conservative
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                                                     Conservative
     18
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50.0%;
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chaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
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Pred. No. 56;
4; Mismatches
                                               Score 41; DB 2; Length 575; Pred. No. 56; ; Mismatches 2; Indels
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GGCX OR GC.
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Science 254:1634-1636(1991).
-I- FUNCTION: VITAMIN K-DEPENDENT CATERMINAL GLUTAMIC ACID RESIDUES
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SUBUNIT: MAY FORM A HOMODIMER (PROBABLE).
PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: SOME, TO PLANT AND MAMMALIAN LIPOXYGENASES.
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STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Frieschmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
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SEQUENCE OF 127-226 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hut
Pasurvey of the Mycoplasma genitalium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- CATALYTIC ACTIVITY: CTP + phosphatidate = diphosphate + CDP-
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NCBI_TaxID=2097;
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                               544 AA.
                                                                                                                                                                                         Length 305;
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RESULT
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Best Local S
Matches 10
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Spermatophyta; Magnoliophyta; L
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                      IBPS_BOVIN P00975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM SEQUENCE
                                                              MEDLINE=81044408; PubMed=7428928;
Wachter E., Deppner K., Hochstrasser K., Lempart K., Ge
"A new Kunitz-type inhibitor from bovine serum amino ac
determination.";
FEBS Lett. 119:58-62(1980).
-!- FUNCTION: THIS INHIBITOR HAS ACTIVITY VERY SIMILAR
BASIC PROTEASE INHIBITOR FROM BOVINE TISSUES.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN
PIR; A01206; TIBOR.
                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Serum basic protease inhibitor (Serum
Bos taurus (Bovine)
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Panstruga R.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
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TRANSMEM 1
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15-JUL-1999
                                                    HSSP; P00974; 1BPI
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544 AA;
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illarity 40.0%;
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Pred. No.
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red. No. 22;
Mismatches
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(on update)
(um BPI).
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sequence
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PROSITE; PS50279; BPTI_KUNITZ_2; 1
Serine protease inhibitor.
DISULFID 7 57 BY SI
DISULFID 16 40 BY SI
DISULFID 32 53 BY SI
ACT_SITE 17 18 REACT
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_MYCGE
Y415_MYCGE
P47655;
01-FEB-1996
01-FEB-1996
16-OCT-2001
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ACT_SITE
SEQUENCE
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PIR; S45888; S45888.
SGD; S0000236; YBR032W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94378725; PubMed=8091864; Smits P.H.M., de Haan M., Maat C., Grivell L.A.; "The complete sequence of a 33 kb fragment on the right arm of chromosome II from Saccharomyces cerevisiae reveals 16 open reading frames, including ten new open reading frames, five previously identified genes and a homologue of the SCO1 gene."; Yeast 10:S75-S80(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c;
MEDLINE=94378725; Pub
Smits P.H.M., de Haan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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PROSITE; PS00280;
PROSITE; PS50279;
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protein in RPL4A-HMT1 intergenic region.
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REACTIVE BOND.
B9953EBAACF1A4E6 CRC64;
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Mismatches 4:
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                                                                                                  272 AA.
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Matches 5
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TISSUE=Liver;
MEDLINE=90274676; PubMed=2112380;
MEDLINE=90274676; PubMed=2112380;
Sato H., Koiwai O., Tanabe K., Kashiwamata S.;
Sato H., Koiwai O., Tanabe K., Kashiwamata S.;
Isolation and sequencing of rat liver bilirubin and sequencing of rat liver bilirubin possible alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-756993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Frieschmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

-i- SIMILARITY: BELONGS TO THE MG414 / MG415 FAMILY.
                                                                                                                                                                                                                                                                                                                             UD13_RAT STANDARD; PRT; 531 AA.
Q64637;
Q64637;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q16-OCT-2001 (Rel. 40, Last annotation update)
QDP-glucuronosyltransferase 1-3 precursor, microsomal (UDPGT) (UGT1*3) (UGT1-03) (UGT1A3) (B3).
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STRAIN=ATCC 33530
MEDLINE=96026346;
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Bacteria; Firmic
NCBI_TaxID-2097;
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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Firmicutes:
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Rodentia;
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3 POTENTIAL.
2504 MW; A221BAA6185231A4
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Pred. No. 17;
2; Mismatches
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                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                  -dan
                 splicing
                                                                                                                                                                                                                                                                      Euteleostomi;
Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma
                                                                                                                                                                                                                                                                                                                                                (
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                   O.f.
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Matches
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SUBSEQUENT ELIMINATION OF ENDOGENOUS COMPOUNDS.
-1- CATALYTIC ACTIVITY: UDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; D38067; BAA07262.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPHUU
Pfam; PF00201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
CARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene
SIGNAL
                                                                                                                                                                                                                                                                          PKN2_MYXXA STANDARD; PRT; 8
P54736;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                             AXXXW
                                                                                                  SEQUENCE FROM N.A.
STRAIN-DZF1;
MEDLINE-95293229; PubMed-7774814;
Udo H., Munoz-Dorado J., Inouye M., I
"Myxococcus xanthus, a Gram-negative
transmembrane protein serine/threonin
                                                secretion of beta-lactamase by phosphor Genes Dev. 9:972-983(1995).
-!- FUNCTION: REGULATES THE ACTIVITY OF RELATED ENZYMES, BY BLOCKING THEIR
                                                                                                                                                                                                NCBI_TaxID=34;
                                                                                                                                                                                                             myxococcus xanthus.
Bacteria; Proteobacteria; delta
Myxococcales; Cystobacterineae;
                                                                                                                                                                                                                                                     PKN2
                                                                                                                                                                                                                                                                 Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00201; UDPGT; 1. PROSITE; PS00375; UDPGT; 1 Transferase; Glycosyltrans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D38067; BAA07262.1; -
EMBL; M34007; AAA42312.1; A
InterPro; IPR002213; UDPGT.
                                                                                                                                                                                                                                        Myxococcus
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          IN RESPONSE :
SIMILARITY: I
SIMILARITY: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-D-glucuronoside.
SUBCELLULAR LOCATION: Microsomal.
SUBCELLULAR LOCATION: Microsomal.
SUBCELLULAR LOCATION: Microsomal.
ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFE UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AN COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           PCGAVMILY
                                                                                                                                                                                                                                                                                                                                                                                                 PCGAVLAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family; Microsome;
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489
116
139
293
293
431
431
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                         TO AN EXTERNAL SIGNA BELONGS TO THE SER/T
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505
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66.7%;
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                                                                                                                                                                                                                                                                   kinase
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            GUANYLATE
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N-LINKEI
N-LINKEI
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Pred.
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ECB0994C6A2C7CEF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UDP-GLUCURONOSYLTRANSFERASE 1-3.
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                                                                                                                                                                                                                                                                                                                                 PRT;
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Myxo
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IMPORTANCE IN THE CONJUGATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Transmembrane; Signal;
                        HEIR SECRETION BY PHOSPHORYLATION, NAL YET TO BE IDENTIFIED. /THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; DB
No. 32;
                                                                                                                                 Inouye S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tive splicing.
                                                                                                      bacterium, contains a
ne kinase that blocks the
                                                                                                                                                                                                               coccaceae;
                                                                                                                                                                                                                           ivision; Myxobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERENT N-TERMINAL DOMAIN AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENE ENCODES FOR MANY DIFFERENT
                                                                                          horylation.";
                                                                                                                                                                                                                                                                                            update)
                                                                 OF ENDOGENOUS BETA-LACTAMASE OR
            CYCLASE DOMAIN.
                                                                                                                                                                                                                                                                 update)
(EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                   830 AA
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                                                                                                                                                                                                              Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 531;
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IRX6_MOUSE
Q9ER75;
15-JUN-2002 (
15-JUN-2002 (
15-JUN-2002 (
                                                                                                                                                                                                                                                 SEQUENCE FROM M. .... STRAIN=NIH Swiss; TISSUE=Heart; STRAIN=NIH Swiss; TISSUE=Heart; MEDLINE=20499358; Pubmed=11042143; Peters T., Dildrop R., Ausmeier K., Ruether U.; Peters T., Dildrop R., Ausmeier K., Ruether U.; Porganization of mouse Iroquois homeobox genes in the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
BINDING
ACT_SITE
SEQUENCE
   the Europuse by modified
                                                                                                                                            development.";
Genome Res. 10:1435-1462(2000).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE TALE/IRO HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                              suggests a conserved regulation
development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M94857; AAA98813.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRX6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
Iroquois-class homeodomain pro
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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by non-profit institutions as hified and this statement is not rem
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                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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606
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135
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illarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (Mouse).
Metazoa; Chordata; (
…+heria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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annotation update)
protein IRX-6 (Iro
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GUANYLATE CYCLASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
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Mismatches
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                                                                                                                                                                                                                                                              vertebrate
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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Matches
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HSSP; P40424; 1B72.
MGD; MGI:1927642; Irx6.
InterPro; IPR001064; Crystallin.
InterPro; IPR001356; Homeobox.
InterPro; IPR003893; Iroquois_homeo.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Nuclear protein.
DNA_BIND 143 205 HOMEOBOX.
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16-OCT-2001 ()
16-OCT-2001 ()
Hypothetical ()
AF2332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou 1 Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
or send a
                                                                                                                                                                        reducing archaeon Archaeoglobus 1 Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49
MEDLINE-98049343; Pubmed-9389475;
                                                                    modified and this statement
entities requires a license
or send an email to license
                                                                                              use by non-
modified and
                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobaceae;
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YN32_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARCFU
   Hypothetical SEQUENCE 1
                          EMBL; AE000943; AAB88920.1;
TIGR; AF2332; -
                                                                                                                                         between
                                                                                                                                                                                                                         Venter J.
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Similarity 45.0%;
9; Conservative
                                                                                                            non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                           lobus fulgidus.
Euryarchaeota;
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256
438 AA;
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  l protein;
148 AA; 1
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(Rel. 40, Last annotation
protein AF2332.
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                                                                   license agreement license@isb-sib.cl
                                                                                                            institutions
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   Complete 7384 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobi;
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Pred.
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8F7FF3
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32;
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me.
76CF10669F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaeoglobales;
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RESULT 12
UPK_LACLA
ID UPK_L
AC Q9CDM
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Best Local S
Matches 7
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SEQUENCE
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TRANSMEM
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococ lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-i- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl phosphate. Confers resistance to bacitracin (By similarity).
-i- CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÙPK OR BACA OR LL2192.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative undecaprenol kinase (EC 2.7.1.66) (Bacitracin
                                                                                                                                                                                                                                                                       modified and this statement is not removentities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CDM7;
                                                                                                                                                                                                                Transferase;
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                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                 EMBL; AE006448; AAK06290.1;
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    57
                          8
                                                                                                                                                                                                                                                                                                                                                              phosphate.
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
MISCELLANEOUS: Bacitracin is thought to be involved in inhibition of peptidoglycan synthesis by sequestering undecaprenyl diphosphate reducing the pool of lipid carrier available.
SIMILARITY: BELONGS TO THE UPK FAMILY.
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    SVVVLYFHK
                          AVMILYFHK 16
                                                                                                                                                                                                                        PF02673; BacA;
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Similarity 41.2%;
7; Conservative
                                                 Similarity 6; Conserv
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7
                                                                                                                                                                                                                                                                                                         non-profit
                                                                                           118
158
195
229
284
                                                 Conservative
                                                                                                                                                                                                                Kinase;
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66
108
137
180
217
251
283
32079
                                                                                                                                                                                                                                                                                                         institutions as long
                                                                                                                                                                                                                            BacA.
                                                            38.2%;
                                                                                                                                                                                                                Antibiotic resistance;
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                                                 Score 39; DB
Pred. No. 26;
3; Mismatches
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83ABD014DDDBB14E CRC64;
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No.
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13;
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26;
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                                                                      Length 284;
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YBL2_SFV3L STANI
ID YBL2_SFV3L STANI
AC P27403; Q88191;
DT 01-AUG-1992 (Rel. 2
DT 01-NOV-1995 (Rel. 3
DT 15-JUL-1998 (Rel. 3
CO NCBI_TaxID-11644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92124734; PRO N.A.
RX MEDLINE-9
      RESULT
YURO_B/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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MEDLINE=92124734; Publ
Renne R., Friedl E., S
Neumann-Haefelin D.;
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032156;
15-DEC-1998 (
15-DEC-1998 (
15-JUN-2002 (
Hypothetical
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Kunst F., Ogasawar
Azevedo V., Berter
Entian
Fritz (
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BACSU
 Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03274; Foamy_BEL;
Hypothetical protein.
SEQUENCE 388 AA; 44527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M74895; AAA47800.1;
EMBL; M74895; AAA47797.1;
PIR; E40820; WMLJBT.
InterPro; IPR004956; Foamy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 186:597-608(1992)
                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
Bacteria; Firmicu
                                                                                                                                                                                                                               STRAIN-168;
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                      precursor
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l ABC transporter extracellular binding protein yuro
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                                                                                                                                                                          PubMed=9384377;
ra N., Moszer I.
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S., Schweizer M.
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No. 35;
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RESULT 15
KIN2_YEAST
ID KIN2_Y
AC P13186
DT 01-JAN
DT 15-DEC
DT 30-MAY
DE Prote1
GN KIN2 O
OS Saccha
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N2_YEASI

KIN2_YEAST

P13186; Q12384;

P13186; Q12384;

T 01-JAN-1990 (Rel. 13, Created)

T 15-DEC-1998 (Rel. 37, Last sequence update)

T 30-MAY-2000 (Rel. 39, Last annotation update)

Protein kinase KIN2 (EC 2.7.1.-).

KIN2 OR YLR096W OR L8004.3.

Saccharomyces cerevisiae (Baker's yeast).

Saccharomyces cerevisiae (Baker's yeast).

Saccharomyces; Saccharomycetaceae; Saccharomyces
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SubtiList; BG14001; yuro.
InterPro; IPR000567; SBP_bac_1.
Pfam; PF01547; SBP_bacterial_1; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01037; SBP_BACTERIAL_1; FALSE_NEG.
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pp1 G., Guy B.J., Haga K., F
ert H., Holsappel S., Hosono
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Klein C.,
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DR EMBL; U53876; AAB67540.1; ...
DR SGD; S0004086; KIN2.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR0002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
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Favello A., Fulton L., G
Hallsworth K., Hawkins J
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MEDLINE=87317589; PubMed=2957690;
Levin D.E., Hammond C.I., Ralston R.O
"Two yeast genes that encode unusual |
Proc. Natl. Acad. Sci. U.S.A. 84:6035
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Taich A., Trevaskis E., Vignati D., W
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Gattung S., Greco
J., Hillier L., Ji
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Sreco T., Kirsten J., Kucaba T.,
L., Jier M., Johnson D.,
P., Le T., Mardis E., Menezes S.,
so D., Rifken L., Riles L.,
Wilcox L., Wohldman P., Vaudin M.,
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Q96u33 neurospora
Q95xa9 caenorhabdi
Q8txf2 methanopyru
Q9v2z9 uncultured
O28805 archaeoglob
Q8rgi7 fusobacteri
Q8x231 magnaporthe
Q9g159 ovis aries
Q8s4P5 zea mays (m
Q8yqq0 anabaena sp
Q8rty6 shewanella
Q8rty5 shewanella
Q8rty5 shewanella
O83868 treponema p
Q9f569 escherichia
Q9js29 chlamydia p
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Q46731 escherichia		4	-		Q8suw8 encephalito	Q5016B mycobacteri	Q98203 molluscum c	Q95yz3 leishmania		Q8xtj7 ralstonia s	Q8xry6 ralstonia s	_	_	0			7 lymantria	0	Q9sk02 arabidopsis		thermopla		063548 drosophila	Q53090 rhodobacter	3	Q91667 pseudomonas	Q8z2n3 salmonella	Q8zky5 salmonella

ALIGNMENTS

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RESULT 1
Q96U33
ID Q96U
AC Q96U
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OC Euka
OC Sorc
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RESULT 2
Q95XA9
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Best Local Similarity
Matches 6; Conserv
Q95XA9;
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submitted (OCT-2001) to the
EMBL; AL355930; CAD01121.1;
Hypothetical protein.
SEQUENCE 155 AA; 17483 MY
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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Q96U33;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 17.5 kDa protein.
B208.030.
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                                                                                              EPCGAVVVFPLRNWK
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40.0%;
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the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Score 48; DB 3; Length 155; Pred. No. 1.8; 4; Mismatches 5; Indels
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                326 AA.
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STRAIN-AV19 / DSM 6324 / JCM 9639;

STRAIN-AV19 / DSM 6324 / JCM 9639;

K MEDLINE-21927647; PubMed-11930014;

K Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N. Slesarev A.I., Mezhevaya K.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stette Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kance and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL; AE010365; AAM01936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
"Direct Submission.";
Submitted (SEP-2001) to the E
EMBL; AC093703; AAL00863.1; -
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
Hypothetical protein.
SEQUENCE 326 AA; 37576 MW;
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Q8TXF2;
Q8TXF2;
Q1-JUN-2002 (TrEME
Q1-JUN-2002 (TrEME
Q1-JUN-2002 (TrEME
CO dehydrogenase/e
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Archaea; Euryarchaeota; I
Methanopyrus.
NCBI_TaxID=2320;
[1]
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01-DEC-2001 (TremBirel. 1
01-JUN-2002 (TremBirel. 2
Hypothetical 37.6 kDa pro
                                    Complete SEQUENCE
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CDHD OR MK0722.
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. investigating biology. The C. elegar Science 282:2012-2018(1998).
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Pred. No. 7.8;
1; Mismatches
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SEQUENCE FROM N.A.

MEDLINE-99365980; PubMed-10436927;
Bidle K.A., Kastner M., Bartlett D.H.

"A phylogenetic analysis of microbial methane hydrate containing marine flumargin (ODP site 8928).";

FEMS Microbiol. Lett. 177:101-108(199 EMBL; AF121100; AAD45632.1; -.

HSSP; P11558; 1MRO.

InterPro; IPR003183; MCR_alpha.

Pfam; PF02249; MCR_alpha; 1.

Pfam; PF02249; MCR_alpha; 1.

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SEQUENCE 207 AA; 22546 MW; 4A507E
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01-MAY-2000 (
01-MAY-2000 (
01-OCT-2001 (
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                           []
                                                                                                                                                                                                                                                                                                                                            Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobaceae; Archaeoglobus
NCBI_TaxID=2234;
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Q8RG17;
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Bhattacharyya A., Bartman A., Gardner W.,
Vasieva O., Chu L., Kogan Y., Chaga O., G
Larsen N., D'Souza M., Walunas T., Pusch
Fonstein M., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKA; 1.
Hypothetical protein; Complete
SEQUENCE 222 AA; 25036 MW;
Eukaryota; Fungi; Ascomycota; P
Sordariomycetes incertae sedis;
NCBI_TaxID=148305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence and analysis of the nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
EMBL; AE010543; AAL94512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM STRAIN-ATCC 25586;
STRAIN-ATCC 25586;
MEDLINE-21886394; PubMed-11889109;
MEDLINE-1 V Anderson I., Ivanova N.,
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Bacteria; Fusobacteria;
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InterPro; IPR003661; His_kinA.
InterPro; IPR004359; HIS_KIN_sig
Pfam; PF02518; HATPase_c; 1.
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TIGR; AF1467;
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Nature 390:364-370(1997).
EMBL; AE001001; AAB89779.1; -.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence)
01-JUN-2002 (TrEMBLrel. 21, Last annotate)
Vitamin K-dependent gamma-carboxylase.
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Cetartiodactyla; Run Bovidae; Caprinae; Ovis.
NCBI_TaxID-9940;
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Q8S4P5;
01-JUN-2002
01-JUN-2002
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Enhancer of
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF312035; AAG30935.1; -
InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR000504; RNA_rec_mot.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SEQUENCE 758 AA; 87581 MW; 87F8B58C187B9091 CPCFA.
                                                                                                                                                                                                                                                                                                            Zea mays (Maize).
Eukaryota; Viridiplantae; Strospermatophyta; Magnoliophyta;
Panicoideae; Andropogoneae; Zoncesi_TaxID=4577;
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STRAIN-INA168; TRANSPOSON-OCCAN;
Kito H., Takahashi Y., Sato J.,
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SEQUENCE
            SEQUENCE FROM N.A.

MEDLINE=21948211; PubMed=11950982;
Springer N.M., Danilevskaya O.N.,
Phillips R.L., Kaeppler H.F., Kaep
"Sequence Relationships, Conserved
for Maize Homologs of the Polycomb
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                                              Danilevskaya O.N., Hermon P., Helentjaris T.G., Kaeppler H.F., Kaeppler S.M.; tionships, Conserved Domains, and Expression Patterns
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oup Genes E(z), esc, and E(Pc) ";
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e identified from M. grisea.";
ank/DDBJ databases.
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RESULT 11
Q8RTY6
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AC Q8RTY
DT 01-JU
RF SPHIR
RN (1)
RP SEQUE
RC STRAI
RA FURUS
RA PURUS
RA OKINC
RT "MOLG
RT Deacy
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DR EMBL;
SQ SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sa
Watanabe A., Iriguchi M., Ishikawa A., Kawashima
Kishida Y., Kohara M., Matsumoto M., Matsuno A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M.
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous ni
cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).

EMBL; AP003594; BAB75469.1; -.

Hypothetical protein; Complete proteome.
SEQUENCE 64 AA; 7403 MW; 92AADC7A9C0F8EF8 CR
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Q8YQQ0;
01-MAR-2002
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            "Molecular Cloning and Charles acterium, Deacylase from a Marine Bacterium, J. Biol. Chem. 0:0-0(2002).
EMBL; AB079849; BAB85110.1; -.
SEROUENCE 992 AA; 109848 MW; CE
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EMBL; AF4
SEQUENCE
                                                                                          Okino N.,
                                                                                                                 STRAIN-G8;
                                                                                                     Furusato M.,
                                                                                                                                                         NCBI_TaxID-38313;
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                                                                                                                                  SEQUENCE
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ASR3770.
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AF443597; AAM13421.1; -.
NCE 894 AA; 99979 MW; 9C2B
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Similarity 58.3%;
7; Conservative
                                                                                                                                FROM N.A.
                                                              Ichinose S., Omori A., Ito M.; r Cloning and Characterization of Sphingolipid from a Marine Bacterium, Shewanella alga G8.";
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2 (TrEMBLrel, 20, La
2 (TrEMBLrel. 20, La
11 protein Asr3770.
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ilarity 38.9%;
Conservative
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annotation
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1 A., Kawashima K
1., Matsuno A., M
1., Takazawa M.,
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Nima K., Kimura T
A., Muraki A.,
M., Yamada M.,
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Length 992;
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                                                                                                               "Complete genome sequence of spirochete."; Science 281:375-388(1998). EMBL; AE001259; AAC65853.1; -HSSP; P09980; JUAA.
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STRAIN-NS589;
Sueyoshi N., Furusato P
"Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                              Fraser C.M., Norris S.J., Weinston Dodson R., Gwinn M., Hickey E.K., Sodergren E., Hardham J.M., McLec Khalak H., Richardson D., Howell McDonald L., Artiach P., Bowman C.
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Venter J.C.;
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MEDLINE-98332770;
                                                         Pfam; PF00580; UvrD-helicase;
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Spirochaetales;
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Q9JS29;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
SET domain protein.
CPJ0878 OR CP0991.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID-83558;
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SEQUENCE
MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sampei G., Motomura K., Masuda S., Yamaguchi Teuruya N., Komano T., Mizobuchi K.; "Organization and diversification of plasmid on cleotide sequence of the R721 genome."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-K-12; TRANSPOSON-TN7;
MEDLINE-93015772; PubMed-1400257;
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Plasmid R721
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STRAIN-AR39;
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"Nucleotide sequence of the R721 shufflon.";
J. Bacteriol. 174:7053-7058(1992).
EMBL; AP002527; BAB12599.1; -.
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Nucleic Acids Res. [2]
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SMART; SM00317; SET; 1.
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SEQUENCE 221 AA; 25889
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